

FIG. 1A

1 CACCCTATCC TACACTACTA GGAACCTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCACCCCT GGCTCCCAA ACCCTCCAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGCTC CTCCATCCAC 240
 241 CCAGCGCCCG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTACAA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

FIG. 1B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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FIG. 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

FIG. 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCCTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAACTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

FIG. 2A

1 CACCCTATCC TACACTACTA GGAAC TTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCACCCT GGCTCCCAA ACCCTCCAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTCCT CTCCATCCAC 240
 241 CCAGCGCCCG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTGGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

FIG. 2B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTGGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGA CTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCCGAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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FIG. 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTA TAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTA AAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGA CATGGAACCC ATGATTCTTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

FIG. 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCCTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCA TTTTACAGAC AGGAAAAGTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

FIG. 3A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGTCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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FIG. 3B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 4A

1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 4B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATT ATGTCTTTGT GGGCCAGCTC 960
 299 F F A F T N S S L N P V I Y V F V G Q L 318

 961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F R T K V W E L Y K Q C T P K S L A P I 338

 1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 5A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCAA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 5B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 6A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCAAC 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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FIG. 6B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTG CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATG ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

FIG. 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGA GGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTC TGTCATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAATTT ACATGGCAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTT GAATTTTAA GCAAAGCGT GAAAAAAAG 3240

FIG. 6D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTÀ AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGÀ GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

FIG. 7A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACA ACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTA CTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

FIG. 7B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGACC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCC ATGCATTCCA TTTCTGGAAG TGAATTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

FIG. 8A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAAC TTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA C TACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTG TACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

FIG. 8B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCTGC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGACC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

FIG. 9A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGÀ AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAAC TTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TATGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTA CTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

FIG. 9B

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961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

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FIG. 10A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGATCCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACAATAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

FIG. 10B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

FIG. 11A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATT C AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
 141 V L G D A L V D F S L K L Y H A F S A M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CTTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 11B

961 ACAACATTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 12A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
 141 V L G D A L V D F S L K L Y H A F S A M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 12B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATTGA CCAAACCTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGTAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 13A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F A E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
 141 V L G D A L V D F S L K L Y H A F S A M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 13B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 14A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGGAATG 540
 141 V L G D A L V D F S L K L Y H A F S G M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTCAGCA TCGCCAGCCT CTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 14B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCTGTG TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAATTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 15A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTCTCTC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
 141 V L G D A L V D F S L K L Y H A F S A M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTGAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGGAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 15B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
 461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGACC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 16

1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTG AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGAATACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T E E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188
 601 CACGTCCAGA AGGTGACAGA CTTGATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

FIG. 17

1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTTC CCAGCCCTGG CAGGCGGCTC TGTACCATTTC CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGA CTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCACCGA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T E E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C E K A 188
 601 CACGTCCAGA AGGTGACAGA CTTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

FIG. 18

1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCTCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT T CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGT TTTG ACGACGAAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CTTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCCACCA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T Q E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188
 601 CACGTCCAGA AGGTGACAGA CTTGATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

FIG. 19

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BRB1_MOUSE MASQ...SLKLQPSNQSQAPPNITSCEGAPEAWDLLCRVLPGFVITICFFGLLGNLLVLS
BRB1_RAT MASE.VLLELQPSNRSLOAPANITSCESALEDWDLLYRVLPGFVITICFFGLLGNLLVLS
BRB1_HUMAN MASSWPPLELQSSNQSQLFPPONATACDPAPEAWDLLHRVLPPTFIISICFFGLLGNLFVLL
BRB1_RABIT MASQ...CPLELQPSNQSQAPPNATSCSGAPDAWDLHRLPTFIIAIFTLGLLGNSFVLS

BRB1_MOUSE FFLLPWRRWW...QQRQRRLTIAEIYLANLAASDLVFVLGLPFWAENIGNRFNWPFGS DL
BRB1_RAT FFLLPWRQWWQQRQRQRRLTIAEIYLANLAASDLVFVLGLPFWAENIGNRFNWPFGTDL
BRB1_HUMAN VFLLP.....RRQLNVAEIYLANLAASDLVFVLGLPFWAENIGNRQFNWPFGALL
BRB1_RABIT VFLLA.....RRRLSVAEIYLANLAASDLVFVLGLPFWAENIGNRQFDWPFGAAL

BRB1_MOUSE CRVVS GVIKANLFISIFLVVAISQDRYRLVYPMTSWGNRRRRQAQVTCLLIWVAGGLLS
BRB1_RAT CRVVS GVIKANLFISIFLVVAISQDRYRLVYPMTSWGYRRRRQAQATCLLIWVAGGLLS
BRB1_HUMAN CRVINGVIKANLFISIFLVVAISQDRYRLVHVPMA SGRRRRQAQVTCLLIWVAGGLLS
BRB1_RABIT CRVINGVIKANLFISIFLVVAISQDRYSVLVHVPMA SRRRRQAQATCALIWVAGGLLS

BRB1_MOUSE TPTFLLRSVKVVPDLNISACILLFPHEAWHFVRMVELNVLGFLPLAAILFFNYHILASL
BRB1_RAT IPTFLLRSVKVVPDLNVSACILLFPHEAWHFARMVELNVLGFLPLAAILFFNYHILASL
BRB1_HUMAN IPTFLLRSIQAVPDLNISACILLFPHEAWHFARIVELNVLGFLPLAAILFFNYHILASL
BRB1_RABIT TPTFVLRSVRAVPDLNVSACILLFPHEAWHILRMVELNVLGFLPLAAILFFNYHILASL

*

BRB1_MOUSE RGQKEASRTRCGGPKDSKTMGLILTLVASFLVCWAPYHFFAFLEFLVQVRVIQDCFWKEL
BRB1_RAT RGQKEASRTRCGGPKGSKTTGLILTLVASFLVCWCPYHFFAFLEFLVQVRVIQDCSWKEI
BRB1_HUMAN RTREEVSRTRVRGPKDSKTTALILTLVVAFLVCWAPYHFFAFLEFLVQVQAVRGCFWEEF
BRB1_RABIT RRRGERVPSRCGGPRDSKSTALILTLVASFLVCWAPYHFFAFLECLWQVHAIGGCFWEEF

*

BRB1_MOUSE TDLGLQLANFFAFVNSCLNPIIYVFAG LFKTRVLGTL~~~~~
BRB1_RAT TDLGLQLANFFAFVNSCLNPIIYVFAG LLKTRVLGTL~~~~~
BRB1_HUMAN IDLGLQLANFFAFVNSCLNPVIYVFVG LFR TKVWELYKQCTPKSLAPVSSSRKELFQL
BRB1_RABIT TDLGLQLSNFSAFVNSCLNPVIYVFVG LFR TKVWELCQCSPPSLAPVSSSRKELWG

BRB1_MOUSE ~~~~
BRB1_RAT ~~~~
BRB1_HUMAN FWRN
BRB1_RABIT FWRN

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FIG. 20

BRB2_MOUSE ~~~~~MPCSWKLLGFISVHE.PMPTAASFGIEMFNVTTOVLGSALNGTUSKDN.CPDTEW
 BRB2_RAT MDRSSLCP.KTQAVMAFW.GPGCHLSTCIEMFNITTOALGSAHNGTFSEVN.CPDTEW
 BRB2_RABIT ~~~~~MLNITSOVLAPALNGSVSSSCCPNTEW
 BRB2_CAVPO ~~~~~MFNITSOV..SALNATHAOGNSCLDAEW
 BRB2_HUMAN ~~~~~MFSPWKISMFISSVREDSVPTTASFADMLNVTLO..CPTLNGTFAQ.SKCPQVEW

BRB2_MOUSE WSWLNAIQAPFLWVLFLLAALENIFVLSVFFLHKNSCTVAEIYLGNLAAADLILACGLPF
 BRB2_RAT WSWLNAIQAPFLWVLFLLAALENIFVLSVFFLHKNSCTVAEIYLGNLAAADLILACGLPF
 BRB2_RABIT SGWLNVIQAPFLWVLFVLATLENIFVLSVFFLHKSSCTVAEIYLGNLAAADLILACGLPF
 BRB2_CAVPO WSWLNNTIQAPFLWVLFVLAVLENIFVLSVFFLHKSSCTVAEIYLGNLAAADLILACGLPF
 BRB2_HUMAN LGWLNNTIQAPFLWVLFVLATLENIFVLSVFFLHKSSCTVAEIYLGNLAAADLILACGLPF

BRB2_MOUSE WAITIANNFDWVFGVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMGMGRMRGVR
 BRB2_RAT WAITIANNFDWVFGVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMGMGRMRGVR
 BRB2_RABIT WAITIANHFDWVFGVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMGMGRMRGVR
 BRB2_CAVPO WAITIANNFDWVFGVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMGMGRMRGVR
 BRB2_HUMAN WAITISNNFDWVFGVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMGMGRMRGVR

BRB2_MOUSE WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGHNVACVIVYPSRSWEVFTNVLLNLVG
 BRB2_RAT WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGHNVACVIVYPSRSWEVFTNVLLNLVG
 BRB2_RABIT WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGHNVACVIVYPSRSWEVFTNVLLNLVG
 BRB2_CAVPO WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGHNVACVIVYPSRSWEVFTNVLLNLVG
 BRB2_HUMAN WAKLYSLVIWGCTLLLSSPMLVFRTMKDYRDEGHNVACVIVYPSRSWEVFTNVLLNLVG

BRB2_MOUSE FLLPLSVITFCTVRIMQVLRNEMKKFKEVQTERKATVVLAVLGLFVVCWLPFQISTFL
 BRB2_RAT FLLPLSVITFCTVRIMQVLRNEMKKFKEVQTERKATVVLAVLGLFVVCWLPFQISTFL
 BRB2_RABIT FLLPLSVITFCTVQIMQVLRNEMKKFKEIQTERRATVVLAVLGLFVVCWLPFQISTFL
 BRB2_CAVPO FLLPLSVITFCTVQIMQVLRNEMKKFKEIQTERRATVVLAVLGLFVVCWLPFQISTFL
 BRB2_HUMAN FLLPLSVITFCTVQIMQVLRNEMKKFKEIQTERRATVVLAVLGLFVVCWLPFQISTFL

BRB2_MOUSE DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYVLCQ
 BRB2_RAT DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYVLCQ
 BRB2_RABIT DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYVLCQ
 BRB2_CAVPO DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYVLCQ
 BRB2_HUMAN DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYVLCQ

*

BRB2_MOUSE K GCMGEPVQMENSMTLRTSISVERQIHKLQDWAGKKQ~~~~~
 BRB2_RAT K GCMGESVQMENSMTLRTSISVERQIHKLQDWAGNKQ~~~~~
 BRB2_RABIT K GCMGLEPVQAESSMTLRTSISVERQIHKLPEWTRSSQ~~~~~
 BRB2_CAVPO S GCVSEPAQSENSMTLRTSISVERQIHKLQDWARSSEGTTPPGLL
 BRB2_HUMAN K GCRSEPIQMENSMTLRTSISVERQIHKLQDWAGSEKQ~~~~~

FIG. 21A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCNA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCNTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I X L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCNNGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V X G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 21B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCNGCTC 960
299 F F A F T N S S L N P V I Y V F V G X L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 22A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTNCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TMTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

FIG. 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

FIG. 23A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GCGAAGGGG AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F X E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGNAATG 540
 141 V L G D A L V D F S L K L Y H A F S X M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

FIG. 23B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATTGA CCAAACCTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTCCTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

FIG. 24

1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT T CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGA CTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCNA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T X E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAA ATCCTGCCTA ATGATGAGTG CMAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C X K A 188
 601 CACGTCCAGA AGGTGACAGA CTTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

FIG. 25A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCC GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGTCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 25B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 26A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 26B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 27A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCAATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCAAC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I V L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 27B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082.

FIG. 28A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCAAC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R K E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCAGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 28B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 29A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCACCC 60
 1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
 281 I C W L P F Q I S T F L D T L H R L G I 300

FIG. 29B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTÀ CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAAC TÀGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CTTTTATGT AACATGAAGT 2040

FIG. 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CTTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCCTGACCA ATCCAACCTT GAATTTTAAA GCAAAAAGCGT GAAAAAAAAG 3240

FIG. 29D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAA CAGGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC C TATGCATGGT GTAGATGCC C TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

FIG. 30A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCCACC 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCCT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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FIG. 30B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATTÀ CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCCTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTÀ ATAAAGGTTÀ AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTÀ TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

FIG. 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 30D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

FIG. 31A

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1  ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC 60
1  M F S P W K I S M F L S V R E D S V P T 20

61  ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21  T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41  T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61  P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81  V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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FIG. 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K E G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATT CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

FIG. 31C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 31D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

FIG. 32A

1	CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA	60
61	GGGAAAGTCATTTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTTGCTGTAAGTCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCAGTTCG	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTTGAAGAGATTAAACCATTTATATGAACATCTTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATGGATGCCTCCCTGCTCATTT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

FIG. 32B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTTCAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTTCTGCAGCCACACCTAAGCATTAAATCCATTGGTCTTCTGTCCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

FIG. 32C

1741	CTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTCAGACCTCCTTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTTTCTTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGG	2580
2581	TATAGAAAATATAAGATGATAAAGATATCATTTAAATGTCAAACTATGACTCTGTTCAGA	2640

FIG. 32D

2641	AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC	2700
2701	AGTATTTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT	2760
2761	TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAAT	2820
2821	GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTC	2880
2881	GATCTTGATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACGGTGTAGC	2940
2941	TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA	3000
3001	CATGCTTTCTTCACAGTAACTCAGTTCAGTACTATGGTGATTTGCCTACAGTGATGTTT	3060
3061	GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG	3120
3121	GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA	3180
3181	AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAACTCATTTCTAC	3240
3241	TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAAGTGTATGTTACCCCTCTGAAGTGGGT	3300
3301	ACCCAGTCTCTTAAATCTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG	3360
3361	CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAAA	3405

FIG. 33A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 33B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTGCGGATCAAATTCTTCTCTGCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 34A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCTACGCCATGCTTTCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCAAAGACTTTTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 34B

841	CCTAACCAAGGCCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTGCGGATCAAATCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 35A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGCGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 35B

841	CCTAACCAAGGCAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 36A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGTTGTCAGNGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCCAAAGACTTNTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 36B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCCTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 37A

1	CGCCCAACCCAAAGTTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTTAGTCTA	60
61	GGGAAAGTCATTCAAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTTGCTGTAAGTCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTTGGACAAGTTTAACCAACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTTACTACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

FIG. 37B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCCTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCTTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTTCAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAA	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCCAC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTC TAATGATTACTCATTTCATTTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

FIG. 37C

1741	CTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAGAATTCTTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTTTAAAGTAAAAAATCAGATGATTCTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAACGTGTCTGATATCATTCCTAGAACTGAAAGTTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTCAGACCTCCTTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGG	2580
2581	TATAGAAAATATAAGATGATAAAGATATCATTAATGTCAAAACTATGACTCTGTTTCAGA	2640

FIG. 37D

2641 AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC 2700
 2701 AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT 2760
 2761 TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAAT 2820
 2821 GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTTG 2880
 2881 GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAAC TGGTGTAGC 2940
 2941 TGCAAGGATTGAGAAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA 3000
 3001 CATGCTTTCTTCACAGTAAC TCAAGTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT 3060
 3061 GGAATCGATCATGCTTTCTTCAAGGTGACAGGTC TAAAGAGAGAAGAATCCAGGGAACAG 3120
 3121 GTAGAGGACATTGCTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA 3180
 3181 AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAACTCATTTCTAC 3240
 3241 TGTTCCTCTAACTGTGGAGTGAATGGAAATTC CAACTGTATGTTACCCCTCTGAAGTGGGT 3300
 3301 ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGT TGGAGCAGTGCTGAGCACAAAG 3360
 3361 CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAAA 3405

FIG. 38A

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1  ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTN GTGAGGNCTC CGTGCCCACC 60
1  M F S P W K I S M F L S V X E X S V P T 20

61  ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCCAC TCTTAACGGG 120
21  T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41  T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61  P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81  V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCCT GAGTGTCACT 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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FIG. 38B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K X G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATTa CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTa ATAAAGGTTa AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTa TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCa 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTa TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

FIG. 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

FIG. 38D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAA CAGGTGAAAG AAGAAGTAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAACTGTGC CACACATGGT GAATGAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

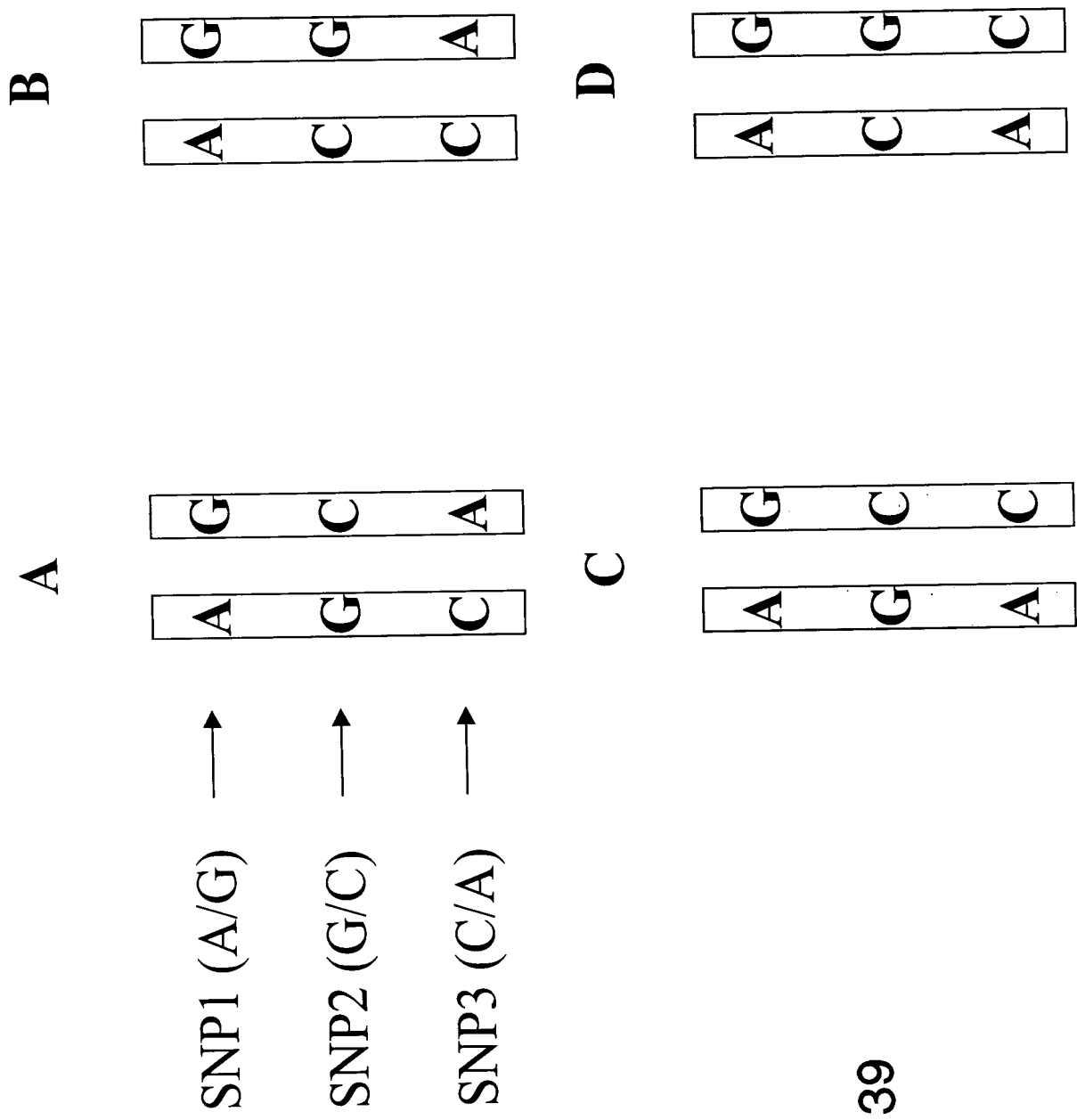


FIG. 39

FIG. 40

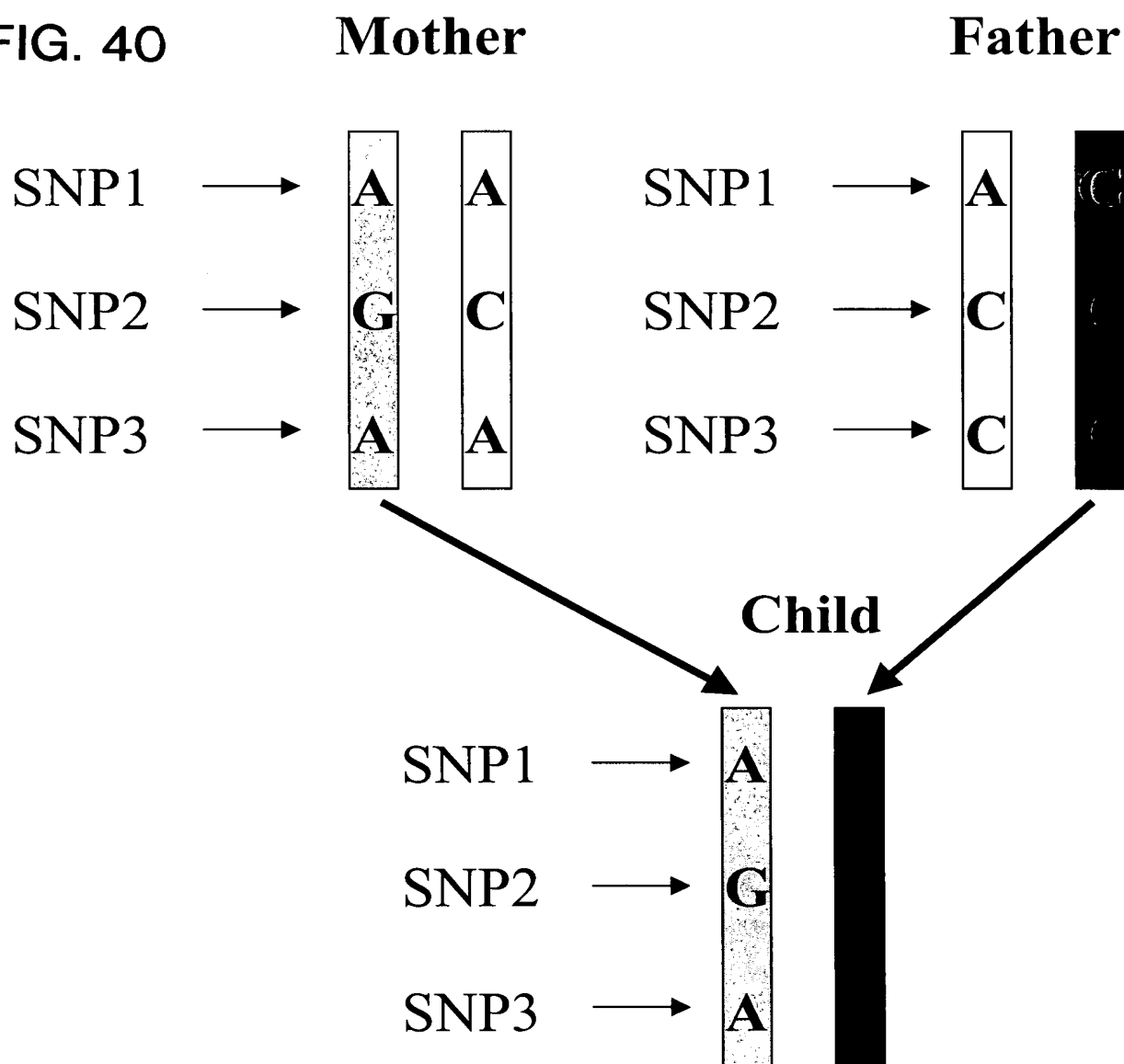


FIG. 41A

1 CACCCTATCC TACACTACTA GGAAC TTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCAACCCT GGCTCCCAA ACCCTCCAA ACAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCACCCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGGAAGGAGC CCTCCCTCTC TCCCTTGTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

FIG. 41B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCTG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCCGAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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FIG. 41C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCAGACA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTAAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCCT CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

FIG. 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCCTC 3120
3121 ACCTTGTTGT GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAACTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

FIG. 42A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACTGTC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V Q G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

FIG. 42B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

FIG. 43A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGCCTC CGTGCCCACC 60
1 M F S P W K I S M F L S V R E A S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCCT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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FIG. 43B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCCTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

FIG. 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAÀ GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAAGCGT GAAAAAAAAG 3240

FIG. 43D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

FIG. 44A

1	ATGCATCTTATCGACTACCTGCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGGCGCCTACGCCATGCTTTCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGAGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTTCATTTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 44B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACGACGTTTCGCGATCAAATTCCTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 45A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGGCGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACATGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T <u>C</u> V G	140
421	AGTGCTCTGTTCTCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTTCATTTCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

FIG. 45B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAAC TTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAAC TGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTTCGCGATCAAATTCCTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCACGAAACCATAG	1284
421	V V D P T K P *	428

FIG. 46A

1 CACCCTATCC TACACTACTA GGAAC TTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCACCCT GGCTCCCAA ACCCTCCAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTC CTGGGGCCAC ACAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

FIG. 46B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTTCG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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FIG. 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTA TAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGTTGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGCG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

FIG. 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCCTC 3120
3121 ACCTTGTTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAACTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

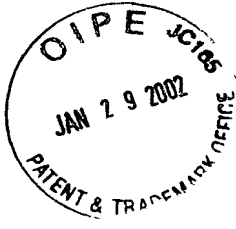


Table III

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) +12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) +12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) +12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) +12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) +12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) +12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) +12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) +12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (2 of 2)

[illegible]

Table V (1 of 2)

[illegible]

Table V (2 of 2)

[illegible]

Table VI

GENE DESCRIPTION	HGNC ID	SNP ID	CONTIG NUM	CONTIG POS	REF_AA	ALT_AA	EXON	MUTATION TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO.)	FLANK (SEQ ID NO.)	REFSEQ_FLANK REF (SEQ ID NO.)
Aminopeptidase P (membrane-bound)	XPINPEP2	AE100s1	1	127	P	P	Exon20	Silent	0	CCC	CCG	ALB6394.1	607	4	37	100
Bradykinin Receptor B1	BOKRB1	AE103s1	6	307	R	Q	Exon2	Missense	0	CGG	CAG	NP_000701.1	317	6	60	123
Bradykinin Receptor B1	BOKRB1	AE103s2	4	273	P	P	Exon2	Silent	0	CCG	CCA	NP_000701.1	41	10	61	124
Tachykinin Receptor 1	TACR1	AE106s1	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001049.1	111	16	81	144
Tachykinin Receptor 1	TACR1	AE106s2	2	769	I	I	Exon2	Silent	1	ATC	ATA	NP_001049.1	154	18	82	145
Tachykinin Receptor 1	TACR1	AE106s7	6	511	S	S	Exon5	Silent	1	TGG	TCA	NP_001049.1	379	20	87	150
C1 Esterase Inhibitor	C1INH	AE105s3	5	366	S	S	Exon7	Silent	0	AGC	AGT	NP_000553.1	406	24	90	153
C1 Esterase Inhibitor	C1INH	AE105s4	7	568	V	A	Exon3	Missense	0	GTT	GCT	NP_000553.1	56	26	91	154
C1 Esterase Inhibitor	C1INH	AE105s5	7	697	A	G	Exon3	Missense	0	GCA	GGA	NP_000553.1	159	28	92	155
C1 Esterase Inhibitor	C1INH	AE105s6	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000553.1	480	30	93	156
Kallikrein 1 (membrane-associated)	KLK1	AE107s1	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	196	34	94	157
Kallikrein 1 (membrane-associated)	KLK1	AE107s3	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159
Bradykinin Receptor B1	BOKRB1	AE103s6	1	67	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	558	579	611
Bradykinin Receptor B1	BOKRB1	AE103s7	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	558	580	612
Bradykinin Receptor B1	BOKRB1	AE103s8	1	296	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	560	581	613
Bradykinin Receptor B1	BOKRB1	AE103s9	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	582	614
Bradykinin Receptor B2	BOKRB2	AE104s19	7	339	R	C	Exon2	Missense	1	CCT	TGT	NP_000614.1	14	564	584	616
Bradykinin Receptor B2	BOKRB2	AE104s24	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000614.1	311	566	589	621
Bradykinin Receptor B2	BOKRB2	AE104s25	4	1048	G	E	Exon3	Missense	1	GCG	GAG	NP_000614.1	354	568	590	622
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	N	N	Exon18	Silent	1	AAT	AAC	AA78220.1	690	643	601	633
Protease Inhibitor 4	PI4	AE110s2	2	528	F	F	Exon2	Silent	0	TTC	TTT	NP_006006.1	233	574	603	635
Protease Inhibitor 4	PI4	AE110s5	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_006006.1	199	576	606	638

Table VIIA

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	P14	ACE2
Coriell 24 panel	NA14905	African American	x	x	x	x	x			
Coriell 24 panel	NA14922	African American								
Coriell 24 panel	NA14923	African American	x	x	x	x	x			
Coriell 24 panel	NA14924	African American	x	x	x	x	x			
Coriell 24 panel	NA14925	African American	x	x	x	x	x			
Coriell 24 panel	NA14932	African American	x	x	x	x	x			
Coriell 24 panel	NA14933	African American	x	x	x	x	x			
Coriell 24 panel	NA14934	African American	x	x	x	x	x			
Coriell 24 panel	NA 17201	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17202	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17203	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17204	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17205	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17206	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17207	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA17208	Caucasian	x	x	x	x	x			
Coriell 24 panel	NA00576	Chinese	x	x	x	x	x			
Coriell 24 panel	NA03433	Chinese	x	x	x	x	x			
Coriell 24 panel	NA06090	Chinese	x	x	x	x	x			
Coriell 24 panel	NA07426	Chinese	x	x	x	x	x			
Coriell 24 panel	NA02345b	Japanese	x	x	x	x	x			
Coriell 24 panel	NA11589	Japanese	x	x	x	x	x			
Coriell 24 panel	NA14819	Japanese	x	x	x	x	x			
Coriell 24 panel	NA04535	Japanese	x	x	x	x	x			
Corell 8 panel	NA14672	African American								
Corell 8 panel	NA14682	African American								
Corell 8 panel	NA14683	African American								
Corell 8 panel	NA14696	African American								
Corell 8 panel	NA14698	African American								
Corell 8 panel	NA14700	African American								
Corell 8 panel	NA14704	African American								
HD 50 AA panel	NA1850	African American								
HD 50 AA panel	3382	African American								
HD 50 AA panel	3725	African American								
HD 50 AA panel	6865	African American								
HD 50 AA panel	7754	African American								
HD 50 AA panel	10251	African American								
HD 50 AA panel	10378	African American								
HD 50 AA panel	12931	African American								
HD 50 AA panel	13294	African American								
HD 50 AA panel	14439	African American								
HD 50 AA panel	14441	African American								
HD 50 AA panel	14454	African American								
HD 50 AA panel	14464	African American								

Table VIIB

DNA panel	Coriell Catalog #	Sample Description	XPNEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50 AA panel	14537	African American	x							
HD 50 AA panel	14583	African American	x							
HD 50 AA panel	14681	African American	x							
HD 50 AA panel	14687	African American	x							
HD 50 AA panel	14697	African American	x							
HD 50 AA panel	14699	African American	x							
HD 50 AA panel	14720	African American	x							
HD 50 AA panel	14746	African American	x							
HD 50 AA panel	14754	African American	x							
HD 50 AA panel	14755	African American	x							
HD 50 AA panel	14771	African American	x							
HD 50 AA panel	14772	African American	x							
HD 50 AA panel	14783	African American	x							
HD 50 AA panel	14826	African American	x							
HD 50 AA panel	14837	African American	x							
HD 50 AA panel	14862	African American	x							
HD 50 AA panel	14863	African American	x							
HD 50 AA panel	14864	African American	x							
HD 50 AA panel	14892	African American	x							
HD 50 AA panel	14893	African American	x							
HD 50 AA panel	14894	African American	x							
HD 50 AA panel	14895	African American	x							
HD 50 AA panel	14897	African American	x							
HD 50 AA panel	14900	African American	x							
HD 50 AA panel	14901	African American	x							
HD 50 AA panel	14903	African American	x							
HD 50 AA panel	14904	African American	x							
HD 50 AA panel	14905	African American	x							
HD 50 AA panel	14922	African American	x							
HD 50 AA panel	14923	African American	x							
HD 50 AA panel	14924	African American	x							
HD 50 AA panel	14925	African American	x							
HD 50 AA panel	14932	African American	x							
HD 50 AA panel	14933	African American	x							
HD 100 CAU panel	NA 17201	Caucasian	x							
HD 100 CAU panel	17202	Caucasian	x							
HD 100 CAU panel	17203	Caucasian	x							
HD 100 CAU panel	17204	Caucasian	x							
HD 100 CAU panel	17205	Caucasian	x							
HD 100 CAU panel	17206	Caucasian	x							
HD 100 CAU panel	17207	Caucasian	x							
HD 100 CAU panel	17208	Caucasian	x							
HD 100 CAU panel	17209	Caucasian	x							
HD 100 CAU panel	17210	Caucasian	x							

Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian	x							
HD 100 CAU panel	17212	Caucasian	x							
HD 100 CAU panel	17213	Caucasian	x							
HD 100 CAU panel	17214	Caucasian	x							
HD 100 CAU panel	17215	Caucasian	x							
HD 100 CAU panel	17216	Caucasian	x							
HD 100 CAU panel	17217	Caucasian	x							
HD 100 CAU panel	17218	Caucasian	x							
HD 100 CAU panel	17219	Caucasian	x							
HD 100 CAU panel	17220	Caucasian	x							
HD 100 CAU panel	17221	Caucasian	x							
HD 100 CAU panel	17222	Caucasian	x							
HD 100 CAU panel	17223	Caucasian	x							
HD 100 CAU panel	17224	Caucasian	x							
HD 100 CAU panel	17225	Caucasian	x							
HD 100 CAU panel	17226	Caucasian	x							
HD 100 CAU panel	17227	Caucasian	x							
HD 100 CAU panel	17228	Caucasian	x							
HD 100 CAU panel	17229	Caucasian	x							
HD 100 CAU panel	17230	Caucasian	x							
HD 100 CAU panel	17231	Caucasian	x							
HD 100 CAU panel	17232	Caucasian	x							
HD 100 CAU panel	17233	Caucasian	x							
HD 100 CAU panel	17234	Caucasian	x							
HD 100 CAU panel	17235	Caucasian	x							
HD 100 CAU panel	17236	Caucasian	x							
HD 100 CAU panel	17237	Caucasian	x							
HD 100 CAU panel	17238	Caucasian	x							
HD 100 CAU panel	17239	Caucasian	x							
HD 100 CAU panel	17240	Caucasian	x							
HD 100 CAU panel	17241	Caucasian	x							
HD 100 CAU panel	17242	Caucasian	x							
HD 100 CAU panel	17243	Caucasian	x							
HD 100 CAU panel	17244	Caucasian	x							
HD 100 CAU panel	17245	Caucasian	x							
HD 100 CAU panel	17246	Caucasian	x							
HD 100 CAU panel	17247	Caucasian	x							
HD 100 CAU panel	17248	Caucasian	x							
HD 100 CAU panel	17249	Caucasian	x							
HD 100 CAU panel	17250	Caucasian	x							
HD 100 CAU panel	17251	Caucasian	x							
HD 100 CAU panel	17252	Caucasian	x							
HD 100 CAU panel	17253	Caucasian	x							
HD 100 CAU panel	17254	Caucasian	x							

Table VIID

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17255	Caucasian	x							
HD 100 CAU panel	17256	Caucasian	x							
HD 100 CAU panel	17257	Caucasian	x							
HD 100 CAU panel	17258	Caucasian	x							
HD 100 CAU panel	17259	Caucasian	x							
HD 100 CAU panel	17260	Caucasian	x							
HD 100 CAU panel	17261	Caucasian	x							
HD 100 CAU panel	17262	Caucasian	x							
HD 100 CAU panel	17263	Caucasian	x							
HD 100 CAU panel	17264	Caucasian	x							
HD 100 CAU panel	17265	Caucasian	x							
HD 100 CAU panel	17266	Caucasian	x							
HD 100 CAU panel	17267	Caucasian	x							
HD 100 CAU panel	17268	Caucasian	x							
HD 100 CAU panel	17269	Caucasian	x							
HD 100 CAU panel	17270	Caucasian	x							
HD 100 CAU panel	17271	Caucasian	x							
HD 100 CAU panel	17272	Caucasian	x							
HD 100 CAU panel	17273	Caucasian	x							
HD 100 CAU panel	17274	Caucasian	x							
HD 100 CAU panel	17275	Caucasian	x							
HD 100 CAU panel	17276	Caucasian	x							
HD 100 CAU panel	17277	Caucasian	x							
HD 100 CAU panel	17278	Caucasian	x							
HD 100 CAU panel	17279	Caucasian	x							
HD 100 CAU panel	17280	Caucasian	x							
HD 100 CAU panel	17281	Caucasian	x							
HD 100 CAU panel	17282	Caucasian	x							
HD 100 CAU panel	17283	Caucasian	x							
HD 100 CAU panel	17284	Caucasian	x							
HD 100 CAU panel	17285	Caucasian	x							
HD 100 CAU panel	17286	Caucasian	x							
HD 100 CAU panel	17287	Caucasian	x							
HD 100 CAU panel	17288	Caucasian	x							
HD 100 CAU panel	17289	Caucasian	x							
HD 100 CAU panel	17290	Caucasian	x							
HD 100 CAU panel	17291	Caucasian	x							
HD 100 CAU panel	17292	Caucasian	x							
HD 100 CAU panel	17293	Caucasian	x							
HD 100 CAU panel	17294	Caucasian	x							
HD 100 CAU panel	17295	Caucasian	x							

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Table VIII(1 of 2)

Table VIII(2 of 2)

GENE DESCRIPTION	HGNC ID	SNP ID	EXON	REVCOMP	PCR Amplicon Name	Target Name	PCR Left primer		PCR Left primer (SEQ ID NO:)	PCR Right primer		PCR Right primer (SEQ ID NO:)
							GCCTCTGATCTGGTGTGTTGTC	CTGTGATCTGGCTATCTCTGCG				
Bradykinin Receptor B1	BDKRB1	AE10386	Exon3	0	AE10386p10	U48231_X2.12a	GCCTCTGATCTGGTGTGTTGTC	CTGTGATCTGGCTATCTCTGCG	707	CTGTGATCTGGCTATCTCTGCG	739	
Bradykinin Receptor B1	BDKRB1	AE10387	Exon3	0	AE10386p10	U48231_X2.2a	GCCTCTGATCTGGTGTGTTGTC	CTGTGATCTGGCTATCTCTGCG	708	CTGTGATCTGGCTATCTCTGCG	740	
Bradykinin Receptor B1	BDKRB1	AE10388	Exon3	0	AE10386p10	U48231_X2.2a	GCCTCTGATCTGGTGTGTTGTC	CTGTGATCTGGCTATCTCTGCG	709	CTGTGATCTGGCTATCTCTGCG	741	
Bradykinin Receptor B1	BDKRB1	AE10389	Exon3	0	AE10386p10	U48231_X2.2a	GCCTCTGATCTGGTGTGTTGTC	CTGTGATCTGGCTATCTCTGCG	710	CTGTGATCTGGCTATCTCTGCG	742	
Bradykinin Receptor B2	BDKRB2	AE10418	Intron1 or Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	711	AGATCGACGACGAGAGGAGG	743	
Bradykinin Receptor B2	BDKRB2	AE10419	Exon2	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	712	AGATCGACGACGAGAGGAGG	744	
Bradykinin Receptor B2	BDKRB2	AE10420	5' Flank	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	713	AGATCGACGACGAGAGGAGG	745	
Bradykinin Receptor B2	BDKRB2	AE10421	5' Flank	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	714	AGATCGACGACGAGAGGAGG	746	
Bradykinin Receptor B2	BDKRB2	AE10422	5' Flank	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	715	AGATCGACGACGAGAGGAGG	747	
Bradykinin Receptor B2	BDKRB2	AE10423	5' Flank	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	716	AGATCGACGACGAGAGGAGG	748	
Bradykinin Receptor B2	BDKRB2	AE10424	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	717	AGATCGACGACGAGAGGAGG	749	
Bradykinin Receptor B2	BDKRB2	AE10425	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	718	AGATCGACGACGAGAGGAGG	750	
Bradykinin Receptor B2	BDKRB2	AE10426	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	719	AGATCGACGACGAGAGGAGG	751	
Bradykinin Receptor B2	BDKRB2	AE10427	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	720	AGATCGACGACGAGAGGAGG	752	
Bradykinin Receptor B2	BDKRB2	AE10428	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	721	AGATCGACGACGAGAGGAGG	753	
Bradykinin Receptor B2	BDKRB2	AE10429	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	722	AGATCGACGACGAGAGGAGG	754	
Bradykinin Receptor B2	BDKRB2	AE10430	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	723	AGATCGACGACGAGAGGAGG	755	
Bradykinin Receptor B2	BDKRB2	AE10431	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	724	AGATCGACGACGAGAGGAGG	756	
Bradykinin Receptor B2	BDKRB2	AE10432	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	725	AGATCGACGACGAGAGGAGG	757	
Bradykinin Receptor B2	BDKRB2	AE10433	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	726	AGATCGACGACGAGAGGAGG	758	
Bradykinin Receptor B2	BDKRB2	AE10434	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	727	AGATCGACGACGAGAGGAGG	759	
Bradykinin Receptor B2	BDKRB2	AE10435	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	728	AGATCGACGACGAGAGGAGG	760	
Bradykinin Receptor B2	BDKRB2	AE10436	Exon3	1	AE10425p66	BDKRB2_X3.5a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	729	AGATCGACGACGAGAGGAGG	761	
Bradykinin Receptor B2	BDKRB2	AE10437	Exon16	1	AE10947p18	BDKRB2_X3.2a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	730	AGATCGACGACGAGAGGAGG	762	
Protease inhibitor 4	P4	AE11081	Intron1	0	AE11081p18	P4_X2a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	731	GCGAGGCGAGGATCTCTTATAG	782	
Protease inhibitor 4	P4	AE11082	Exon2	0	AE11082p22	P4_X2a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	732	GCGAGGCGAGGATCTCTTATAG	783	
Protease inhibitor 4	P4	AE11083	Intron2	0	AE11082p22	P4_X3a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	733	GCGAGGCGAGGATCTCTTATAG	784	
Protease inhibitor 4	P4	AE11084	Intron2	0	AE11082p22	P4_X3a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	734	GCGAGGCGAGGATCTCTTATAG	785	
Protease inhibitor 4	P4	AE11085	Exon1	0	AE11081p18	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	735	GCGAGGCGAGGATCTCTTATAG	786	
Protease inhibitor 4	P4	AE11086	5' Flank	0	AE11085p6	P4_X1.2a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	736	GCGAGGCGAGGATCTCTTATAG	787	
Protease inhibitor 4	P4	AE11087	5' Flank	0	AE11085p6	P4_X1.2a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	737	GCGAGGCGAGGATCTCTTATAG	788	
Protease inhibitor 4	P4	AE11088	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	738	GCGAGGCGAGGATCTCTTATAG	789	
Protease inhibitor 4	P4	AE11089	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	739	GCGAGGCGAGGATCTCTTATAG	790	
Protease inhibitor 4	P4	AE11090	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	740	GCGAGGCGAGGATCTCTTATAG	791	
Protease inhibitor 4	P4	AE11091	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	741	GCGAGGCGAGGATCTCTTATAG	792	
Protease inhibitor 4	P4	AE11092	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	742	GCGAGGCGAGGATCTCTTATAG	793	
Protease inhibitor 4	P4	AE11093	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	743	GCGAGGCGAGGATCTCTTATAG	794	
Protease inhibitor 4	P4	AE11094	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	744	GCGAGGCGAGGATCTCTTATAG	795	
Protease inhibitor 4	P4	AE11095	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	745	GCGAGGCGAGGATCTCTTATAG	796	
Protease inhibitor 4	P4	AE11096	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	746	GCGAGGCGAGGATCTCTTATAG	797	
Protease inhibitor 4	P4	AE11097	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	747	GCGAGGCGAGGATCTCTTATAG	798	
Protease inhibitor 4	P4	AE11098	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	748	GCGAGGCGAGGATCTCTTATAG	799	
Protease inhibitor 4	P4	AE11099	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	749	GCGAGGCGAGGATCTCTTATAG	800	
Protease inhibitor 4	P4	AE11100	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	750	GCGAGGCGAGGATCTCTTATAG	801	
Protease inhibitor 4	P4	AE11101	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	751	GCGAGGCGAGGATCTCTTATAG	802	
Protease inhibitor 4	P4	AE11102	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	752	GCGAGGCGAGGATCTCTTATAG	803	
Protease inhibitor 4	P4	AE11103	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	753	GCGAGGCGAGGATCTCTTATAG	804	
Protease inhibitor 4	P4	AE11104	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	754	GCGAGGCGAGGATCTCTTATAG	805	
Protease inhibitor 4	P4	AE11105	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	755	GCGAGGCGAGGATCTCTTATAG	806	
Protease inhibitor 4	P4	AE11106	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	756	GCGAGGCGAGGATCTCTTATAG	807	
Protease inhibitor 4	P4	AE11107	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	757	GCGAGGCGAGGATCTCTTATAG	808	
Protease inhibitor 4	P4	AE11108	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	758	GCGAGGCGAGGATCTCTTATAG	809	
Protease inhibitor 4	P4	AE11109	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	759	GCGAGGCGAGGATCTCTTATAG	810	
Protease inhibitor 4	P4	AE11110	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	760	GCGAGGCGAGGATCTCTTATAG	811	
Protease inhibitor 4	P4	AE11111	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	761	GCGAGGCGAGGATCTCTTATAG	812	
Protease inhibitor 4	P4	AE11112	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	762	GCGAGGCGAGGATCTCTTATAG	813	
Protease inhibitor 4	P4	AE11113	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	763	GCGAGGCGAGGATCTCTTATAG	814	
Protease inhibitor 4	P4	AE11114	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	764	GCGAGGCGAGGATCTCTTATAG	815	
Protease inhibitor 4	P4	AE11115	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	765	GCGAGGCGAGGATCTCTTATAG	816	
Protease inhibitor 4	P4	AE11116	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	766	GCGAGGCGAGGATCTCTTATAG	817	
Protease inhibitor 4	P4	AE11117	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	767	GCGAGGCGAGGATCTCTTATAG	818	
Protease inhibitor 4	P4	AE11118	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	768	GCGAGGCGAGGATCTCTTATAG	819	
Protease inhibitor 4	P4	AE11119	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	769	GCGAGGCGAGGATCTCTTATAG	820	
Protease inhibitor 4	P4	AE11120	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	770	GCGAGGCGAGGATCTCTTATAG	821	
Protease inhibitor 4	P4	AE11121	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	771	GCGAGGCGAGGATCTCTTATAG	822	
Protease inhibitor 4	P4	AE11122	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	772	GCGAGGCGAGGATCTCTTATAG	823	
Protease inhibitor 4	P4	AE11123	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	773	GCGAGGCGAGGATCTCTTATAG	824	
Protease inhibitor 4	P4	AE11124	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	774	GCGAGGCGAGGATCTCTTATAG	825	
Protease inhibitor 4	P4	AE11125	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	775	GCGAGGCGAGGATCTCTTATAG	826	
Protease inhibitor 4	P4	AE11126	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	776	GCGAGGCGAGGATCTCTTATAG	827	
Protease inhibitor 4	P4	AE11127	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	777	GCGAGGCGAGGATCTCTTATAG	828	
Protease inhibitor 4	P4	AE11128	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	778	GCGAGGCGAGGATCTCTTATAG	829	
Protease inhibitor 4	P4	AE11129	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	779	GCGAGGCGAGGATCTCTTATAG	830	
Protease inhibitor 4	P4	AE11130	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	780	GCGAGGCGAGGATCTCTTATAG	831	
Protease inhibitor 4	P4	AE11131	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	781	GCGAGGCGAGGATCTCTTATAG	832	
Protease inhibitor 4	P4	AE11132	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	782	GCGAGGCGAGGATCTCTTATAG	833	
Protease inhibitor 4	P4	AE11133	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	783	GCGAGGCGAGGATCTCTTATAG	834	
Protease inhibitor 4	P4	AE11134	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	784	GCGAGGCGAGGATCTCTTATAG	835	
Protease inhibitor 4	P4	AE11135	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	785	GCGAGGCGAGGATCTCTTATAG	836	
Protease inhibitor 4	P4	AE11136	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	786	GCGAGGCGAGGATCTCTTATAG	837	
Protease inhibitor 4	P4	AE11137	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	787	GCGAGGCGAGGATCTCTTATAG	838	
Protease inhibitor 4	P4	AE11138	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	788	GCGAGGCGAGGATCTCTTATAG	839	
Protease inhibitor 4	P4	AE11139	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	789	GCGAGGCGAGGATCTCTTATAG	840	
Protease inhibitor 4	P4	AE11140	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	790	GCGAGGCGAGGATCTCTTATAG	841	
Protease inhibitor 4	P4	AE11141	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	791	GCGAGGCGAGGATCTCTTATAG	842	
Protease inhibitor 4	P4	AE11142	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	792	GCGAGGCGAGGATCTCTTATAG	843	
Protease inhibitor 4	P4	AE11143	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	793	GCGAGGCGAGGATCTCTTATAG	844	
Protease inhibitor 4	P4	AE11144	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGACGAGAGGAGG	794	GCGAGGCGAGGATCTCTTATAG	845	
Protease inhibitor 4	P4	AE11145	5' Flank	0	AE11081p2	P4_X1.1a	GCGAGGCGAGGAATAGTCT	AGATCGACGAC				

Table IX (1 of 2)

[illegible]

Table IX(2 of 2)

Bradykinin Receptor B2	BKBRB2	AE104928	Exon3	1	BKBRB2_X3-2a	TTCGTGAGACAGGACATGCC	AE104955	785	TATTCGACAAACCACTGTGTCCC	AE104956	817
Bradykinin Receptor B2	BKBRB2	AE104929	Exon3	1	BKBRB2_X3-2b	TTCGTGAGACAGGACATGCC	AE104955	786	TATTCGACAAACCACTGTGTCCC	AE104956	818
Angiotensin Converting Enzyme 2	ACE2	AE10981	Intinr14	1	ACE2_X14a	TTTGTGAAAGAGAGGACATGCC	AE109827	787	ATTTGGGATCTTTGGAGGAAAA	AE109828	819
Angiotensin Converting Enzyme 2	ACE2	AE10982	Intinr12	1	ACE2_X13a	CAGCTGTGTCAAGAGTCTCTCA	AE109931	788	ACATCTGGAAGCCCTCAAAAG	AE109932	820
Angiotensin Converting Enzyme 2	ACE2	AE10983	Intinr13	1	ACE2_X13b	CAGCTGTGTCAAGAGTCTCTCA	AE109931	789	ACATCTGGAAGCCCTCAAAAG	AE109932	821
Angiotensin Converting Enzyme 2	ACE2	AE10984	Intinr2	1	ACE2_X14a	TTTGTGAAAGAGGACATGCC	AE109971	790	TCTTCAGGAAATTTTCAATTTGT	AE109972	822
Angiotensin Converting Enzyme 2	ACE2	AE10985	Intinr18	1	ACE2_X13a	TTTGTGAAAGAGGACATGCC	AE109971	791	TCTTCAGGAAATTTTCAATTTGT	AE109972	823
Angiotensin Converting Enzyme 2	ACE2	AE10986	Exon16	1	ACE2_X18a	GCACACAGGAGAGACACAA	AE109919	792	CTCTCCCATGTCTCTCATCTC	AE109920	824
Angiotensin Converting Enzyme 2	ACE2	AE10987	Exon16	1	ACE2_X18a	GCACACAGGAGAGACACAA	AE109919	793	CTCTCCCATGTCTCTCATCTC	AE109920	825
Protease Inhibitor 4	Pi4	AE11081	Intinr1	0	Pi4_X2a	GATCTGGAGGAGGAGTCTTG	AE110823	794	CACATGTGAGTGTCTGATCTC	AE110824	826
Protease Inhibitor 4	Pi4	AE11082	Exonr2	0	Pi4_X2a	GATCTGGAGGAGGAGTCTTG	AE110823	795	CACATGTGAGTGTCTGATCTC	AE110824	827
Protease Inhibitor 4	Pi4	AE11083	Intinr2	0	Pi4_X3a	CTTTTCACATCATCTGTGGG	AE110827	796	ACTTTGGATGTGCTCATGTTT	AE110828	828
Protease Inhibitor 4	Pi4	AE11084	Intinr2	0	Pi4_X3a	CTTTTCACATCATCTGTGGG	AE110827	797	ACTTTGGATGTGCTCATGTTT	AE110828	829
Protease Inhibitor 4	Pi4	AE11085	Exonr1	0	Pi4_X15a	CTTACGCCATCTTTCCTCTG	AE110919	798	CGTGTGGTGTGGATTTAGCAT	AE110920	830
Protease Inhibitor 4	Pi4	AE11086	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	799	CGGTGGTGTGGATTTAGCAT	AE11098	831
Protease Inhibitor 4	Pi4	AE11087	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	800	CGGTGGTGTGGATTTAGCAT	AE11098	832
Protease Inhibitor 4	Pi4	AE11088	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	801	CGGTGGTGTGGATTTAGCAT	AE11098	833
Protease Inhibitor 4	Pi4	AE11089	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	802	CGGTGGTGTGGATTTAGCAT	AE11098	834
Protease Inhibitor 4	Pi4	AE11090	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	803	CGGTGGTGTGGATTTAGCAT	AE11098	835
Protease Inhibitor 4	Pi4	AE11091	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	804	CGGTGGTGTGGATTTAGCAT	AE11098	836
Protease Inhibitor 4	Pi4	AE11092	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	805	CGGTGGTGTGGATTTAGCAT	AE11098	837
Protease Inhibitor 4	Pi4	AE11093	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	806	CGGTGGTGTGGATTTAGCAT	AE11098	838
Protease Inhibitor 4	Pi4	AE11094	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	807	CGGTGGTGTGGATTTAGCAT	AE11098	839
Protease Inhibitor 4	Pi4	AE11095	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	808	CGGTGGTGTGGATTTAGCAT	AE11098	840
Protease Inhibitor 4	Pi4	AE11096	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	809	CGGTGGTGTGGATTTAGCAT	AE11098	841
Protease Inhibitor 4	Pi4	AE11097	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	810	CGGTGGTGTGGATTTAGCAT	AE11098	842
Protease Inhibitor 4	Pi4	AE11098	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	811	CGGTGGTGTGGATTTAGCAT	AE11098	843
Protease Inhibitor 4	Pi4	AE11099	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	812	CGGTGGTGTGGATTTAGCAT	AE11098	844
Protease Inhibitor 4	Pi4	AE11100	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	813	CGGTGGTGTGGATTTAGCAT	AE11098	845
Protease Inhibitor 4	Pi4	AE11101	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	814	CGGTGGTGTGGATTTAGCAT	AE11098	846
Protease Inhibitor 4	Pi4	AE11102	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	815	CGGTGGTGTGGATTTAGCAT	AE11098	847
Protease Inhibitor 4	Pi4	AE11103	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	816	CGGTGGTGTGGATTTAGCAT	AE11098	848
Protease Inhibitor 4	Pi4	AE11104	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	817	CGGTGGTGTGGATTTAGCAT	AE11098	849
Protease Inhibitor 4	Pi4	AE11105	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	818	CGGTGGTGTGGATTTAGCAT	AE11098	850
Protease Inhibitor 4	Pi4	AE11106	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	819	CGGTGGTGTGGATTTAGCAT	AE11098	851
Protease Inhibitor 4	Pi4	AE11107	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	820	CGGTGGTGTGGATTTAGCAT	AE11098	852
Protease Inhibitor 4	Pi4	AE11108	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	821	CGGTGGTGTGGATTTAGCAT	AE11098	853
Protease Inhibitor 4	Pi4	AE11109	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	822	CGGTGGTGTGGATTTAGCAT	AE11098	854
Protease Inhibitor 4	Pi4	AE11110	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	823	CGGTGGTGTGGATTTAGCAT	AE11098	855
Protease Inhibitor 4	Pi4	AE11111	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	824	CGGTGGTGTGGATTTAGCAT	AE11098	856
Protease Inhibitor 4	Pi4	AE11112	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	825	CGGTGGTGTGGATTTAGCAT	AE11098	857
Protease Inhibitor 4	Pi4	AE11113	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	826	CGGTGGTGTGGATTTAGCAT	AE11098	858
Protease Inhibitor 4	Pi4	AE11114	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	827	CGGTGGTGTGGATTTAGCAT	AE11098	859
Protease Inhibitor 4	Pi4	AE11115	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	828	CGGTGGTGTGGATTTAGCAT	AE11098	860
Protease Inhibitor 4	Pi4	AE11116	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	829	CGGTGGTGTGGATTTAGCAT	AE11098	861
Protease Inhibitor 4	Pi4	AE11117	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	830	CGGTGGTGTGGATTTAGCAT	AE11098	862
Protease Inhibitor 4	Pi4	AE11118	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	831	CGGTGGTGTGGATTTAGCAT	AE11098	863
Protease Inhibitor 4	Pi4	AE11119	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	832	CGGTGGTGTGGATTTAGCAT	AE11098	864
Protease Inhibitor 4	Pi4	AE11120	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	833	CGGTGGTGTGGATTTAGCAT	AE11098	865
Protease Inhibitor 4	Pi4	AE11121	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	834	CGGTGGTGTGGATTTAGCAT	AE11098	866
Protease Inhibitor 4	Pi4	AE11122	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	835	CGGTGGTGTGGATTTAGCAT	AE11098	867
Protease Inhibitor 4	Pi4	AE11123	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	836	CGGTGGTGTGGATTTAGCAT	AE11098	868
Protease Inhibitor 4	Pi4	AE11124	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	837	CGGTGGTGTGGATTTAGCAT	AE11098	869
Protease Inhibitor 4	Pi4	AE11125	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	838	CGGTGGTGTGGATTTAGCAT	AE11098	870
Protease Inhibitor 4	Pi4	AE11126	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	839	CGGTGGTGTGGATTTAGCAT	AE11098	871
Protease Inhibitor 4	Pi4	AE11127	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	840	CGGTGGTGTGGATTTAGCAT	AE11098	872
Protease Inhibitor 4	Pi4	AE11128	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	841	CGGTGGTGTGGATTTAGCAT	AE11098	873
Protease Inhibitor 4	Pi4	AE11129	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	842	CGGTGGTGTGGATTTAGCAT	AE11098	874
Protease Inhibitor 4	Pi4	AE11130	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	843	CGGTGGTGTGGATTTAGCAT	AE11098	875
Protease Inhibitor 4	Pi4	AE11131	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	844	CGGTGGTGTGGATTTAGCAT	AE11098	876
Protease Inhibitor 4	Pi4	AE11132	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	845	CGGTGGTGTGGATTTAGCAT	AE11098	877
Protease Inhibitor 4	Pi4	AE11133	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	846	CGGTGGTGTGGATTTAGCAT	AE11098	878
Protease Inhibitor 4	Pi4	AE11134	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	847	CGGTGGTGTGGATTTAGCAT	AE11098	879
Protease Inhibitor 4	Pi4	AE11135	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	848	CGGTGGTGTGGATTTAGCAT	AE11098	880
Protease Inhibitor 4	Pi4	AE11136	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	849	CGGTGGTGTGGATTTAGCAT	AE11098	881
Protease Inhibitor 4	Pi4	AE11137	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	850	CGGTGGTGTGGATTTAGCAT	AE11098	882
Protease Inhibitor 4	Pi4	AE11138	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	851	CGGTGGTGTGGATTTAGCAT	AE11098	883
Protease Inhibitor 4	Pi4	AE11139	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	852	CGGTGGTGTGGATTTAGCAT	AE11098	884
Protease Inhibitor 4	Pi4	AE11140	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	853	CGGTGGTGTGGATTTAGCAT	AE11098	885
Protease Inhibitor 4	Pi4	AE11141	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	854	CGGTGGTGTGGATTTAGCAT	AE11098	886
Protease Inhibitor 4	Pi4	AE11142	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	855	CGGTGGTGTGGATTTAGCAT	AE11098	887
Protease Inhibitor 4	Pi4	AE11143	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	856	CGGTGGTGTGGATTTAGCAT	AE11098	888
Protease Inhibitor 4	Pi4	AE11144	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	857	CGGTGGTGTGGATTTAGCAT	AE11098	889
Protease Inhibitor 4	Pi4	AE11145	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	858	CGGTGGTGTGGATTTAGCAT	AE11098	890
Protease Inhibitor 4	Pi4	AE11146	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	859	CGGTGGTGTGGATTTAGCAT	AE11098	891
Protease Inhibitor 4	Pi4	AE11147	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	860	CGGTGGTGTGGATTTAGCAT	AE11098	892
Protease Inhibitor 4	Pi4	AE11148	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	861	CGGTGGTGTGGATTTAGCAT	AE11098	893
Protease Inhibitor 4	Pi4	AE11149	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	862	CGGTGGTGTGGATTTAGCAT	AE11098	894
Protease Inhibitor 4	Pi4	AE11150	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	863	CGGTGGTGTGGATTTAGCAT	AE11098	895
Protease Inhibitor 4	Pi4	AE11151	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	864	CGGTGGTGTGGATTTAGCAT	AE11098	896
Protease Inhibitor 4	Pi4	AE11152	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	865	CGGTGGTGTGGATTTAGCAT	AE11098	897
Protease Inhibitor 4	Pi4	AE11153	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	866	CGGTGGTGTGGATTTAGCAT	AE11098	898
Protease Inhibitor 4	Pi4	AE11154	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	867	CGGTGGTGTGGATTTAGCAT	AE11098	899
Protease Inhibitor 4	Pi4	AE11155	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	868	CGGTGGTGTGGATTTAGCAT	AE11098	900
Protease Inhibitor 4	Pi4	AE11156	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	869	CGGTGGTGTGGATTTAGCAT	AE11098	901
Protease Inhibitor 4	Pi4	AE11157	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	870	CGGTGGTGTGGATTTAGCAT	AE11098	902
Protease Inhibitor 4	Pi4	AE11158	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	871	CGGTGGTGTGGATTTAGCAT	AE11098	903
Protease Inhibitor 4	Pi4	AE11159	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	872	CGGTGGTGTGGATTTAGCAT	AE11098	904
Protease Inhibitor 4	Pi4	AE11160	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	873	CGGTGGTGTGGATTTAGCAT	AE11098	905
Protease Inhibitor 4	Pi4	AE11161	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	874	CGGTGGTGTGGATTTAGCAT	AE11098	906
Protease Inhibitor 4	Pi4	AE11162	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	875	CGGTGGTGTGGATTTAGCAT	AE11098	907
Protease Inhibitor 4	Pi4	AE11163	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	876	CGGTGGTGTGGATTTAGCAT	AE11098	908
Protease Inhibitor 4	Pi4	AE11164	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	877	CGGTGGTGTGGATTTAGCAT	AE11098	909
Protease Inhibitor 4	Pi4	AE11165	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	878	CGGTGGTGTGGATTTAGCAT	AE11098	910
Protease Inhibitor 4	Pi4	AE11166	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	879	CGGTGGTGTGGATTTAGCAT	AE11098	911
Protease Inhibitor 4	Pi4	AE11167	5Flank	0	Pi4_X17a	TGGGGGGAGGAAATCGAGTAT	AE11097	880	CGGTGGTGTGGATTTAGCAT	AE11098	912
Protease Inhib											

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPT	ORCHID_SNPT (SEQ ID NO:)
AE100s1	TATCATTTTGGCCCTATGACG	1066	CAGGCTCAGGAGAGGCC	1154	CCTCATCGATGTGCGCTGCTGTCTCC	1242
AE100s10	AACTTCATCATCAGAGTACCAAG	1067	GAGGCAATTTTGTATGAGTCTCTC	1155	GTGTTTGGAAACCTTAGCATGACAC	1243
AE100s11	ATAGAATGACTTCTCTCAGAGGGA	1068	CAGCCTACCTCTCTGACTGGG	1156	TGGAGCCCGAGNCCCTCAGAGCT	1244
AE100s12	TCAGAGAGGAGTGGCTG	1069	GAAGGCGAGCTTACCTTG	1157	AGCCGAGGCCCGCAGAGTTCCTCCA	1245
AE100s13	ATAGAATGACTTCTCTCAGAGGGA	1070	GCTCAGAGGCGGAGAGATGTT	1158	AATGTTTGAGAAAGNCGAGCTTAACCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCTCTGTCTGCTCGAG	1071	GATGGAGGACAGGAG	1159	CCCGGCTCTTCTCTTCANGCNTTTCT	1247
AE100s16	AAGNAGGAGGAGGAGGAA	1072	GTCTAGGATAGAGAGGGGTATAGG	1160	AGAAAAGCTTGCTCAGGCGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGCAGACCCCTCTCA	1073	GATCCAGAGCATCTCTATGAC	1161	TACCTAAATAAATAATAAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATTTGCAGGCGAGG	1074	GTATCTTTTGCAGTTCACTCCC	1162	GCAACAAGTCTCTTTTNCAGACAGTC	1250
AE100s20	TACCACACAGGGBACTGG	1075	GATTCAGGTACTGAGCTCG	1163	AGACTTCACCTCTTGGCANTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCTTAAGGACACACAAATTT	1076	GAGTGGCTCAGGACT	1164	CTGCAATGTTGCTGAAGGTGAAGA	1252
AE100s24	CGGTATCTGATCTCCATCATCT	1077	CCGACCTCGAGTTGGGG	1165	TTNGAGCCTGTGGCTTNCACACAGACT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGAGTTGTTTGAGGAAAG	1078	GAGCCCCAAAAGTGAAGTGA	1166	TTACCCCTTANGGCTGACCTTNCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTTTCAGTTGGCACCA	1079	CAATGGACAGGAGGGG	1167	TCACCTGGCTCTCACCAGAGATTC	1255
AE100s4	TCCTGCTGCTCCCGG	1080	AATATTTGTGACTGATTTACGAGATAG	1168	TATTTGAGNCCACTGACANGGCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTGTCATGAGTGTAGTG	1081	CTTGTGATTTTCATACCTGTGAAA	1169	ACCTTCATAGAGGGTATATAAAG	1257
AE100s7	ATCCAGTAATGGCAAGCCAG	1082	GTGAGCTTAGGGTACAGTTTGT	1170	AAGAGTTTGTGAGGAAAGGTTT	1258
AE100s8	GCAATCTCACGTCTGCTG	1083	CAGCTCTGGGGCAGTA	1171	GTAAAGAGGTCTCNAINGCAGAGGG	1259
AE100s9	AAAACCTAGGAAAGACAGAAACACAC	1084	TTTCAGAGGACTGGCAGGAG	1172	CACAGAGTAGAGAGNATTCACGAAA	1260
AE103s1	AACTTCTTTCGCTTCACTTAACAGCT	1085	GATGAAGATATTGAGCAAGACTTTTAG	1173	CCAGTAATTTATGCTCTTTGTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGAATGTTACCAATT	1086	GACTCTGAGCTCTCTGCTC	1174	ATCTGAAATTTATCCAAGTGGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACGAGTTTCTGCTTAATTG	1087	CTTTGAATAGACAAATAAGTGTARTAAGA	1175	CAGCAGGAAACAAATAACAAGTATC	1263
AE103s14	TGTCATAGCAGCAGCAGGAA	1088	CTGGGAGTTAGCTTAGAAGC	1176	ACAAGTATCGGTAAATGNCCTCTCTTA	1264
AE103s2	TCACAGATGCTCCAGAGCC	1089	CAACAGACAAAGAGTCTCCC	1177	CTGGGACCTGCTGACAGAGTCTGCC	1265
AE103s3	ACTTTTCTGGCGAATTAAACA	1090	ACCCCCCAATCTAGGGA	1178	TGAACCAANANGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGAGAGAAATATCTGGA	1091	CCACGAGAGATGCTGATG	1179	GAGCCCTCTCTCTGCCGTGTCATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGAACATCACCGCT	1092	GTAGTTGAAGAGACGATCGC	1180	AGATCTGAACATCACCGCTCTCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGAGCAATAATGCTGTTTTTTGATAA	1093	CTCACCTGTGCTCTTTG	1181	CACCTGGCAAAATCGNCGGCTCTCCCC	1269
AE104s10	GGTTGGGCTCAGGCTG	1094	GTGGCGTGTGAGCACC	1182	GTNGGAATGACAGGTGAGAGGCCA	1270

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPTT	ORCHID_SNPTT (SEQ ID NO:)
AE104s11	TTGGATGTCGAATGCTTCCTG	1095	GCCCTATGATGCTGTAGATG	1183	TTAACAATPAACAGCNCATGATGCTTT	1271
AE104s12	ATTTCCTCGTTGGATGTGAATG	1096	CGCCCTATGATGCTGTGTA	1184	TAACAGCTCATTCAGTCTTTKACAG	1272
AE104s13	GCCATTGCGGCAGAGCTC	1097	AAAAAAGAGGCTGTGTTTGTA	1185	GGGAGTCTATTTCAGCAGCAGAGCAC	1273
AE104s14	AAGTGAATGATGCTGCGCTT	1098	AAGTGCGCCAGTATGAGC	1186	CCCTAGAAGAGTGTGAAGAAGAAATG	1274
AE104s16	GATCGATGATGAGGAGGAGG	1099	CAGTGTGGGGAAATTCATATCC	1187	ATTCCTTCACTCATNTATTAACAACA	1275
AE104s17	GATGGAAAGATGAGGAGAGG	1100	CATAATGCCCTCTCTCAT	1188	TACGTTGAGGGATGAGCCCCAGGTTT	1276
AE104s18	AGAAGAAAGATGGTTAGATGGCA	1101	CATTGAGTCAGGAGCTCAGCA	1189	ACAGGGGCTGGGGATNGCNAATACAC	1277
AE104s19	TAACTAGTGAAGTCTGAGGATCCCTTT	1102	CACTCTGAGTCCAAATGTTCTCTC	1190	GTGGTGGCACGGAGGCTCTCAC	1278
AE104s2	GAGAGCAATAAATGCTCTGTTTGTATAA	1103	CTCACCTGTGCTGCTGTG	1191	GTCAAGGAGGGGNCACCTGGGCGGG	1279
AE104s20	TTTACACTCCAGGCTGAG	1104	CTCTTCCCAAGATCCACTGG	1192	TTTTTGNAGCCTTAAACACCTTTCTTTC	1280
AE104s21	GGATTTCTTTGTATGCCAGGTAC	1105	CATACATCTCCGAGAAACGG	1193	GCAGAAGTGTCTCTGTTCTCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTGGCGGG	1106	GCAGGATGCGAGAGCTCAG	1194	GAAGTCCCGAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTTAAAGAAACCCAGGG	1107	GTTCCTCGTCCCTGCCCC	1195	CATTCACCAAAAGCTGGATGGC	1283
AE104s27	TCGACCGTCTGCTCGAAC	1108	GAAAGAGAGGAGCCATCTCCA	1196	GCCTTCNGGTGTGTCAGTGCCTCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s3	TTTGCAGGAGGGAATC	1109	CAACCTGCACTCCAGGC	1197	GAGCGAAGGGTGGCTGAGGTCATG	1285
AE104s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGATACAAATGGCTAGGAGCT	1110	GTTCGGACCCCATGTTCTAT	1198	ACCTTTTCTTGATTTTTCACGTGA	1286
AE104s34	ACACTGTGCTTCACACCG	1111	GTACATGTGAGGATCTWTAGCC	1199	GGCTCCCAATCTGATCTGTCTCCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCTGCTGCTCCATATCA	1112	CATCTTGAAGGAATCAAAAGATCA	1200	ACCCACAGCACCTGCTNGACCGTCTC	1288
AE104s4	AGTGAGAGGCTTGGAGTGCA	1113	CTTTGGATGAAAGAGGAAGCA	1201	AGGGTTCCAGGGAGACTGGGATGAGG	1289
AE104s5	TGCAGGGTTCCAGGGAGA	1114	CAAGAGAGGCTGCTTTTGGAT	1202	GCTGGGATGANGYCTGGGTGCTGCT	1290
AE104s6	GCTTCACAACTGTGGAATGTC	1115	CAAGAGGCTGCTCCCGA	1203	GTTCCTGGAGAAAACCTGTGCTG	1291
AE104s7	AACTGTGGCCAGAGGGT	1116	AACCTTTACCCACAGC	1204	CCCCCTCCAAAGTCTWTGCCACAA	1292
AE104s8	ATGTAGCTAGCACCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGGGGAACCTGAGGAGGAGACAG	1293
AE104s9	TATTTCTAGACTCAGTGTCTTTTCTTTATAG	1118	GAAGCTGTGTGAGGTTAAAGG	1206	AAGGTCCTACCTANATNTGAGGCATC	1294
AE105s1	GAGAGGACTCTGAAGGGGG	1119	AGGTCTTCACTCTCTCTCCA	1207	CCAGGCTGTGGGAAAGAAAGGACA	1295
AE1052	ATTGTGACAGAGGTGGGG	1120	CAAACTCAGATTGTGGAGGC	1208	GAGATCCGTAGGAGAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	GGGAAGGAAGTTCGCA	1121	TTGAGTTGTTGTCTGGCA	1209	AAGCTGGAANCCTCNAGGATGGTTCA	1297
AE105s5	TGTTGGGGGATGCTTTGG	1122	GATGCTGAATGGGAAGAG	1210	AAGCTCTACAGGCTTCTCAG	1298
AE105s6	ATCTCTGTGGCCCGACG	1123	CATATCTGCCCCATGAGAC	1211	GGAACTTGTCTGCTGGTCCCGAGACA	1299
AE106s1	TATCAAGGCGCACAGCG	1124	CACAAAGATGGTACTAGCGC	1212	TACTGGGGAAGACAGCGGCGATGGG	1300
AE106s2	ATGCTCTGTGTGGTAGTAGTACG	1125	CATCATACATCCCTCCAGC	1213	CCAGCAGGAGAGCCAGGACCCA	1301
AE106s3	ATACCTGGGGATATTTTGTGCA	1126	CTACACAGGAGAGTCTGTG	1214	CCAGCGCAAGGTGAGCAGCGG	1302
AE106s4	TGCAGAAATTCATCTCGAATGA	1127	CTGTGTGACTCAAAACCAATCACT	1215	AGGTCGACCACTTTTCCCAA	1303
AE106s5	AAAGTGTGCTCGACCTTTTAT	1128	TCAAAATATCAATTTCTTCTATCT	1216	TCCCTATCTTTCGACACTNATGCTGT	1304
AE106s6	TTTGAGTCCMACAGCATGAG	1129	CATGGAAATTCCTCTCATCTG	1217	ACCCATATGACCCCTTTTNGCAAGTCC	1305
AE106s7	ATGGTCTTGGAGTCACTTCTGTG	1130	CCCAGGAGGAGGCCAG	1218	AGAGCAGTNGAGGCTCAGGTCAGGGA	1306

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPTT	ORCHID_SNPTT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTCGTAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAAGTCTGTCTAC	1219	CAAAATCCTCGCTTAATGATGAGTGC	1307
AE107s2	AGCATCGAACCCAGAGAAATTGTATG	1132	CTTCCTCGGCCCTTTTCTC	1220	TCCCTTGNACRCAGAGTCCCATCCC	1308
AE107s3	CTTCCTGTATCATCATCAGATG	1133	CATCAATTTCTCTGGTTCTGATGC	1221	GCTGTGAAGNTCGNGAGTGGCCACCC	1309
AE107s4	ATCGAACCCAGAGAAATTGTATGTGG	1134	GGGAGAAAAAGGGCTTGCA	1222	AAAGCHGGGATGGGGACTCTCTG	1310
AE107s5	ACCTGGACCCACTCGGCT	1135	CGTTTCCCCACCTGCTGG	1223	TGNGGCCACCCAGCTGTGTCA	1311
AE107s6	CCAGTAAAAATCAATGTGCATCC	1136	CAGCTCAGCCGAGTGGG	1224	ATGTGTGTACGTTCTGCCATCACCC	1312
AE109s1	AATAGCTTATCCATAGGAATAGGTTACTTT	1137	GAATTGATTTATTTTGAAGTGCACAGTC	1225	ATCTGGAACTTATAGTNTTGAAGAAGA	1313
AE109s2	GGGGGTTCAAGGGCTTTT	1138	GCAATTTAGCCAGTCAAGAGA	1226	GAGGGTTTCCAGANGTACNTATATTTA	1314
AE109s3	TGGGGCCAAAGGAGACTAG	1139	GCTGAAGACCCAGAACAGAAATTC	1227	AAGTAGACAGGAATGGGTGTGABA	1315
AE109s4	GTGTTGAAACACACATATCTGCAAT	1140	TGGAAAGTTTGTACCCAGATATC	1228	TCATAATCAACNANTMAAANTTAGTAGC	1316
AE109s5	GTGTTCAACTGCAAAATTAAGATAATAACA	1141	ACATGGCAAGAAAGTAAATTTGCTG	1229	GAAATTTTCTGAGAGAAATGCTAA	1317
AE109s6	AACCTAAATCAAGATTTATTCCTCTG	1142	GTTACCAATACACAAATACACAGTATT	1230	CACATGTAAATGACTCAGAAATATG	1318
AE109s7	CCCTCACCCCTTAGATGAAGTAAAA	1143	TTTGAACCAAGAAATCTCTTTAATTT	1231	TTCACTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCCCTCCCTGCTCATTTTG	1232	CTTGTAAAGGCCCATNAATTTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGGATGAG	1145	ATGTGGCGATTGTGCTGG	1233	GGNTGGCACCGAGNTGCAGCCAC	1321
AE110s11	CACCTCTCGCACTCTCA	1146	CATGTGTCTATTGAGGAATTTTG	1234	AACCTCNC CGGNATGCGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAAACTGG	1147	CAGTAGAACTGGTCTTTGTATTTTACC	1235	TNCTTTGGACAGATCTTNATTTAGAAA	1323
AE110s2	CTGTACCTTCTTTTCACTCTCCCTT	1148	GCAGCATCATGGGCCACCC	1236	CCGGAAGTGTGTGTTCTCATCAACATA	1324
AE110s3	AAGGAGGGCTCTGCCAG	1149	GATGCACTCTAGCTTCTGTAAAAAT	1237	GATCCTGGCTTGTTCANTANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAAGCACCTCTCAAGAA	1150	GAATTAGCATATACCAATCATCTGACTCT	1238	GAGGGAAGATTTGTGGAATTTGGTCTAG	1326
AE110s6	GTCAAACTTAATGGCTGAAGTGG	1151	TTTCAGATGAGTTGATTTCTATTAGTGC	1239	AGACCTTAATAATAACTCTGAGGAT	1327
AE110s7	AGGCTCAAACTTAATGGCTGAAA	1152	CACCTCTCTTTTCAGATGAGTTGATTTTC	1240	TAAACATATAAAGCACTCCACAGA	1328
AE110s8	AGAAACTGGAGTATCTCTTTCTTGA	1153	CTGTAGAGTCAAGTAAAGTGGTCTTTG	1241	TATGAAGGTTACCAANTTCTATCCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

Table XI (1 of 3)

SNP_ID	GBS_LEFT (SEQ ID NO.1)	GBS_RIGHT (SEQ ID NO.1)	GBS_RIGHT (SEQ ID NO.1)
AE100s1	TGTAATAACGACGGCCAGTGTATCTCTCTCTCTCTCTCACT	CAGGAAACAGCTATGACGAGAGCTCTGGGGTCTCTGAT	1451
AE100s10	TGTAATAACGACGGCCAGTGGCATTCACAGGTATTCAGT	CAGGAAACAGCTATGACCCACGACGAGCAATCATAT	1452
AE100s11	TGTAATAACGACGGCCAGTGTCTGGGCTTTACCTCTCTC	CAGGAAACAGCTATGACCAAGTCTCAGCAGACATCCA	1453
AE100s12	TGTAATAACGACGGCCAGTGTCTTGCGCTTTACCTCTCTC	CAGGAAACAGCTATGACGGTCTCAGCAGAGACATCCA	1454
AE100s13	TGTAATAACGACGGCCAGTCCAGGTCCAGGATTTACAGAC	CAGGAAACAGCTATGACCAAGTCTCAGCAGAGACATCCA	1455
AE100s14	TGTAATAACGACGGCCAGTACTAGGAACCTTGACACATCCG	CAGGAAACAGCTATGACCATGCAACATACCACAGAGAGG	1456
AE100s15	TGTAATAACGACGGCCAGTCTCCACACCTCTATCTACAG	CAGGAAACAGCTATGACCATGCAACATACCACAGAGAGG	1457
AE100s16	TGTAATAACGACGGCCAGTCCAGATCTTGCCCATCTGC	CAGGAAACAGCTATGACCCCAAGCTAGGAAAAGCCATACC	1458
AE100s17	TGTAATAACGACGGCCAGTCCAGCAGACATATGTGTGATG	CAGGAAACAGCTATGACCTCTGCTCTCTGAGCTCTGTT	1459
AE100s18	TGTAATAACGACGGCCAGTATCCAGGTATGTGGTGCATTC	CAGGAAACAGCTATGACCATAGCGATGTGTTGTGGACTGG	1460
AE100s19	TGTAATAACGACGGCCAGTCCAGGTATGTGGTGCATTC	CAGGAAACAGCTATGACCATAGCGATGTGTTGTGGACTGG	1461
AE100s2	TGTAATAACGACGGCCAGTGTGAAGCCCTTTGACAGAAAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1462
AE100s20	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1463
AE100s21	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1464
AE100s22	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1465
AE100s23	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1466
AE100s24	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1467
AE100s25	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1468
AE100s26	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1469
AE100s27	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1470
AE100s28	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1471
AE100s29	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1472
AE100s30	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1473
AE100s31	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1474
AE100s32	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1475
AE100s33	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1476
AE100s34	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1477
AE100s35	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1478
AE100s36	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1479
AE100s37	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1480
AE100s38	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1481
AE100s39	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1482
AE100s40	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1483
AE100s41	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1484
AE100s42	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1485
AE100s43	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1486
AE100s44	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1487
AE100s45	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1488
AE100s46	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1489
AE100s47	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1490
AE100s48	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1491
AE100s49	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1492
AE100s50	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1493
AE100s51	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1494
AE100s52	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1495
AE100s53	TGTAATAACGACGGCCAGTCTTGAAAGCCCAAGAGAT	CAGGAAACAGCTATGACCTTTGTAAGACCCCACT	1496

Table XI (2 of 3)

SNP_ID	GBS_LEFT (SEQ ID NO:1)	GBS_RIGHT (SEQ ID NO:2)
AE104s11	TGTAATAACGAGCGCCAGTTGTCGGAGAGTTGTAAACAAATGCT	CAGGAAACAGCTATGACCGAGGCTGTGTTTGTTCACACA
AE104s12	TGTAATAACGAGCGCCAGTGCATCTACACAAACCTCATCCA	CAGGAAACAGGCTATGACCGGAGCTGTGTTTGTTCACACA
AE104s13	TGTAATAACGAGCGCCAGTCATCTACACCACTAGAGGC	CAGGAAACAGCTATGACCTCGGAGGAGAAACAGGTGAA
AE104s14	TGTAATAACGAGCGCCAGTTAGCTCTCTCAGTTGTTAGCCC	CAGGAAACAGCTATGACCATTTCTTAATCGGTCTTGCCCA
AE104s16	TGTAATAACGAGCGCCAGTAATAAGAGAGGCTGTGACCCAC	CAGGAAACAGCTATGACCTCTAGAACTATAGCGCCAGCAG
AE104s17	TGTAATAACGAGCGCCAGTCAACACATGACCCCAAGTTTAT	CAGGAAACAGCTATGACCGCCACTTTGTTTCTACTCTCCA
AE104s18	TGTAATAACGAGCGCCAGTGAAGAAATCCCTTTGACTCAC	CAGGAAACAGCTATGACCAACAAAGCTCTGAGCAATGTGTGCTTC
AE104s19	TGTAATAACGAGCGCCAGTTGTTTCTCAACTGTGTGTC	CAGGAAACAGCTATGACCAACAGCTTTTGCCAAACAGGAATA
AE104s20	TGTAATAACGAGCGCCAGTGTGTTCTTTAAAGAGGCGCTG	CAGGAAACAGCTATGACCGCGCCACCCCAATAAGCTACTGA
AE104s21	TGTAATAACGAGCGCCAGTATGATGAGCGAGGCTTCT	CAGGAAACAGCTATGACCAATGTTTGTAAAGTCTCTCGCC
AE104s22	TGTAATAACGAGCGCCAGTTTGGATGTATAAGTATAACAGTGGC	CAGGAAACAGCTATGACCTTGAGCAAACTGTAGAGAACGC
AE104s23	TGTAATAACGAGCGCCAGTCTTCAGCACTGTGATCTAC	CAGGAAACAGCTATGACCAATGAGAAATCTTCCTGCAAGAG
AE104s24	TGTAATAACGAGCGCCAGTTCTCCATCTGAATGGGTTCTG	CAGGAAACAGCTATGACCAAGATGACAGAGTTTCAAGG
AE104s25	TGTAATAACGAGCGCCAGTCAAGCAACTGTCTCTCAATCCT	CAGGAAACAGCTATGACCAATCAACAGATTCGCTCTCT
AE104s26	TGTAATAACGAGCGCCAGTGCATCTCTTGTGTCATCAGTGA	CAGGAAACAGCTATGACCAAGACTCTGCAACCAATCACTAA
AE104s27	TGTAATAACGAGCGCCAGTCTCTCAACAGCACTTCAATTT	CAGGAAACAGCTATGACCGGTGATATGGACAGCAGAAG
AE104s28	TGTAATAACGAGCGCCAGTTCTCTCAATAGCTCTCTG	CAGGAAACAGCTATGACCGTCTACTGTAATGTGAGGCA
AE104s29	TGTAATAACGAGCGCCAGTCTCTGAGCACTGTGATCTCT	CAGGAAACAGCTATGACCTTGGAATAAAAGAGAGGAGCA
AE104s3	TGTAATAACGAGCGCCAGTGGCAATATCACCACTTTCAA	CAGGAAACAGCTATGACCGGAACTCAAGACTCAAGTGGG
AE104s30	TGTAATAACGAGCGCCAGTCCCAATCACTGATCTCTCTCA	CAGGAAACAGCTATGACCTGAGTCAAGGAGCTCAGCAGT
AE104s31	TGTAATAACGAGCGCCAGTCTGTCATCTCAATGGAGTTGTT	CAGGAAACAGCTATGACCAATTCATATTTCAACCAAGCG
AE104s32	TGTAATAACGAGCGCCAGTCTGACCTCAATGGAGCTTTGT	CAGGAAACAGCTATGACCTATTGSCAACCACTCTGTCCC
AE104s33	TGTAATAACGAGCGCCAGTCTCTCTGCTCTATCACA	CAGGAAACAGCTATGACCTATTGCAACCACTCTGTCCC
AE104s34	TGTAATAACGAGCGCCAGTCTCTCTGCTCTATCACA	CAGGAAACAGCTATGACCTATTGCAACCACTCTGTCCC
AE104s35	TGTAATAACGAGCGCCAGTCTCTGACCTTTGAAGACATGGCC	CAGGAAACAGCTATGACCTACTCTGATGGAAGAGAGGTC
AE104s36	TGTAATAACGAGCGCCAGTTGTAGCTAGCAGCCCTTTGCTT	CAGGAAACAGCTATGACCAACAGCTTTGGAGGAGCAATTT
AE104s4	TGTAATAACGAGCGCCAGTGAATCCAAAGAGATGTAGGC	CAGGAAACAGCTATGACCGCACTTACAGATTTGTAGGC
AE104s5	TGTAATAACGAGCGCCAGTGAATCCAAAGAGATGTAGGC	CAGGAAACAGCTATGACCGCCAGCTTACAGGAGTGGAG
AE104s6	TGTAATAACGAGCGCCAGTCTCTCTCTTTTCAATCCAA	CAGGAAACAGCTATGACCAACCACTCAATCTAGTCTT
AE104s7	TGTAATAACGAGCGCCAGTGTGCGCAACCAATCTAGTGAG	CAGGAAACAGCTATGACCAACCACTCTAGTGAGGAGAG
AE104s8	TGTAATAACGAGCGCCAGTGTCTCTCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE104s9	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s1	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s2	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s3	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s4	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s5	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s6	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s7	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s8	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE105s9	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s1	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s2	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s3	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s4	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s5	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s6	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA
AE106s7	TGTAATAACGAGCGCCAGTGTGCGCAATCTCTCTACCCCA	CAGGAAACAGCTATGACCAACCACTCTCTCTACCCCA

Table XI (3 of 3)

SNP_ID	GBS_LEFT (SEQ ID NO.1)	GBS_RIGHT (SEQ ID NO.2)	GBS_RIGHT (SEQ ID NO.3)
AE106s8	TGTA AAAACGACGGCAGCTATGGAATTTCTGTTCCTCCCTACAT	CAGGAAACAGCTATGACCCCTTCTCTCTCTCCCTACAT	1543
AE106s9	TGTA AAAACGACGGCAGCTCTTAAGACGACGAGGAGTG	CAGGAAACAGCTATGACCCACACATATGTGGCCAGTGAGAT	1544
AE107s1	TGTA AAAACGACGGCAGCTAATTTGTAATGTGGGGCGAGACT	CAGGAAACAGCTATGACCGTGAAGCAGATATGCTGTGTAG	1545
AE107s2	TGTA AAAACGACGGCAGCTCTGACAGAGCCCTGCTGATAC	CAGGAAACAGCTATGACCAATTTTGAGGTCCACACACTGG	1546
AE107s3	TGTA AAAACGACGGCAGCTCCGACCTGTTTGTTCATGTAGT	CAGGAAACAGCTATGACCGGAATATGAGACTATGAAACCGG	1547
AE107s4	TGTA AAAACGACGGCAGCTCTGACAGAGCTGCTGCTATAC	CAGGAAACAGCTATGACCAAGCTGTCTCAGCTTCTGGACG	1548
AE107s5	TGTA AAAACGACGGCAGCTCCCTTACCCCCAGTAATAATCAA	CAGGAAACAGCTATGACACACTCTCAGCTCTCAGACCTTTC	1549
AE107s6	TGTA AAAACGACGGCAGCTGCGCTCAGAGAGCTGTCTTAT	CAGGAAACAGCTATGACCTTGTCTGTCTGCACTGTCTAC	1550
AE109s1	TGTA AAAACGACGGCAGCTTGACGAGAGTCAATGTAAAGGA	CAGGAAACAGCTATGACCACTGCAGCACTACAAAGCTCAAG	1551
AE109s2	TGTA AAAACGACGGCAGCTCAAGATGTGACGAGCTGCCC	CAGGAAACAGCTATGACCGACCACTACAACAATTTGGGTGG	1552
AE109s3	TGTA AAAACGACGGCAGTAATGTGCAGCTGTCCACATAG	CAGGAAACAGCTATGACCACTGATGTATTAAGCCACTGC	1553
AE109s4	TGTA AAAACGACGGCAGCTCTGACAGAAATAAACCACTGA	CAGGAAACAGCTATGACCTTTCAGCAAAAATTTCCATTTGT	1554
AE109s5	TGTA AAAACGACGGCAGTCTTTCCTGCGATTTATCTGGG	CAGGAAACAGCTATGACCTTCGACAGTGGGGAACTTAAC	1555
AE109s6	TGTA AAAACGACGGCAGCTTGGCCATAGTGTGAATCTTGC	CAGGAAACAGCTATGACCCGAGTGGCTTAATTTGAAACCA	1556
AE109s7	TGTA AAAACGACGGCAGTGCACACAGAGAAACACACAA	CAGGAAACAGCTATGACCTCCGACAGTGTCTCTCTATCC	1557
AE109s8	TGTA AAAACGACGGCAGCTGTGATCTGCTGTGTGT	CAGGAAACAGCTATGACCGAGTGGCTTAATTTGAAACCA	1558
AE109s9	TGTA AAAACGACGGCAGTCTTTCACAAATGCGATTCTT	CAGGAAACAGCTATGACCTTCTCTGGGCTTTTCAG	1559
AE110s1	TGTA AAAACGACGGCAGCTCAGCACTGTATCCCAAGA	CAGGAAACAGCTATGACCTTGTATCTCATCTGATAGACC	1560
AE110s10	TGTA AAAACGACGGCAGCTCTGTGTGTATCCCAAGA	CAGGAAACAGCTATGACCTCTGCTTGGGAACAGATGAG	1561
AE110s11	TGTA AAAACGACGGCAGCTCTGTGTGTATCCCAAGA	CAGGAAACAGCTATGACCCCACTCAATCTTCTCCCTGAGT	1562
AE110s12	TGTA AAAACGACGGCAGCTCTGTGTGTATCCCAAGA	CAGGAAACAGCTATGACCAAGCACTATGTTTGGAGAGAT	1563
AE110s2	TGTA AAAACGACGGCAGTATCTGGAGCACTGTTTCTG	CAGGAAACAGCTATGACCTTTGGCTTGTGTAGGAGAT	1564
AE110s3	TGTA AAAACGACGGCAGTCTTTCACATCCATTTCTGGG	CAGGAAACAGCTATGACCTGACGACTTACTTTGATGCC	1565
AE110s4	TGTA AAAACGACGGCAGTCAAGGAAGCAACACTCTGAAG	CAGGAAACAGCTATGACCGAGGCTGTCAACCTTATCAG	1566
AE110s5	TGTA AAAACGACGGCAGTCTGACAAAATTCCTGATGA	CAGGAAACAGCTATGACCGAGGTTGTCTCAACCTTATCAG	1567
AE110s6	TGTA AAAACGACGGCAGTCTGTGTGTACGGGGTAACA	CAGGAAACAGCTATGACCCCAACAGAGAGAGAAATGAG	1568
AE110s7	TGTA AAAACGACGGCAGTAACTGGGTACCAATTTCTATCCC	CAGGAAACAGCTATGACCTTAGCTAGCACATATCCCAAGCA	1569
AE110s8	TGTA AAAACGACGGCAGTATTTGGGTGTGATGAAGACC	CAGGAAACAGCTATGACCGTGTTCACCACTCTTCCAGCC	1570
AE110s9	TGTA AAAACGACGGTGAAGGTTTGCATGCTGTGTAGT	CAGGAAACAGCTATGACCTTAAGCTAGCTCTGCCCAAGTTG	1571

Table XII

Sample Description

Race	Cases			Controls		
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total
Blacks	11	10	21	32	19	51
Caucasians	12	22	34	38	69	107
Other	0	1	1	0	1	1
Total	23	33	56	70	89	159
						72
						141
						2
						215

Table XIII

Candidate Angioedema Susceptibility Genes

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

Table XIV
Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A _a ¹	Copies of Rare Allele	Odds Ratio (OR) ²	OR Lower 95% CL	OR Upper 95% CL	p(a) ³
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300 0.0251	Asymptotic Exact	A,T	1	3.41 3.37	1.3238 1.2261	8.7969 10.2718	0.28
KLK1	AE107s2	Blacks	7.50	2	0.0062 0.0062	Asymptotic Exact	C,T	1	5.64 5.64	1.4211 1.2422	22.3807 34.7611	0.09
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF	0.28
	Angioedema-like		11.39	2	0.0022	Exact		2	10.82	1.3105	+INF	0.22
	Overall		10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709	0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.